STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/665,671_

Source: _1FW16_

Date Processed by STIC: _12/3/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/665,671_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 12/03/2005
PATENT APPLICATION: US/10/665,671   TIME: 09:47:08

Input Set : **A:\4987 US.txt**
Output Set: **N:\CRF4\12032005\J665671.raw**

```
 3 <110> APPLICANT: ANDERSEN, Mark R.
 4        HUNKAPILLER, Michael W.
 5        LIVAK, Kenneth J.
 6        SPIER, Eugene G.
 7        WENZ, Michael H.
 9 <120> TITLE OF INVENTION: Methods and Compositions for Detecting Targets
11 <130> FILE REFERENCE: 4987 US
13 <140> CURRENT APPLICATION NUMBER: US 10/665,671
14 <141> CURRENT FILING DATE: 2003-09-19
16 <150> PRIOR APPLICATION NUMBER: US 60/412,225
17 <151> PRIOR FILING DATE: 2002-09-19
19 <160> NUMBER OF SEQ ID NOS: 25
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 49
25 <212> TYPE: DNA
26 <213> ORGANISM: Human
28 <400> SEQUENCE: 1
29 ttgcctgctc gacttagatc aaaggagacg cggctgcttt cagcctcat          49
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 49
34 <212> TYPE: DNA
35 <213> ORGANISM: Human
37 <400> SEQUENCE: 2
38 ttgcctgctc gacttagagg gtcacagtag gtggtgcttt cagcctcac          49
41 <210> SEQ ID NO: 3
42 <211> LENGTH: 33
43 <212> TYPE: DNA
44 <213> ORGANISM: Human
46 <400> SEQUENCE: 3
47 ggggatagtg gctgcatcac tggatagcga cgt                          33
50 <210> SEQ ID NO: 4
51 <211> LENGTH: 49
52 <212> TYPE: DNA
53 <213> ORGANISM: Human
55 <400> SEQUENCE: 4
56 ttgcctgctc gacttagatc aaaggagacg cggcagtggt tttccaacg          49
59 <210> SEQ ID NO: 5
60 <211> LENGTH: 51
61 <212> TYPE: DNA
62 <213> ORGANISM: Human
64 <400> SEQUENCE: 5
65 ttgcctgctc gacttagagg gtcacagtag gtggacagtg gttttccaac a       51
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 68 <210> SEQ ID NO: 6
 69 <211> LENGTH: 32
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Human
 73 <400> SEQUENCE: 6
 74 tgaacacacc gggtatcact ggatagcgac gt                          32
 77 <210> SEQ ID NO: 7
 78 <211> LENGTH: 18
 79 <212> TYPE: DNA
 80 <213> ORGANISM: Human
 82 <400> SEQUENCE: 7
 83 ttgcctgctc gacttaga                                          18
 86 <210> SEQ ID NO: 8
 87 <211> LENGTH: 18
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Human
 91 <400> SEQUENCE: 8
 92 acgtcgctat ccagtgat                                          18
 95 <210> SEQ ID NO: 9
 96 <211> LENGTH: 15
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Human
100 <400> SEQUENCE: 9
101 ccgcgtctcc tttga                                             15
104 <210> SEQ ID NO: 10
105 <211> LENGTH: 16
106 <212> TYPE: DNA
107 <213> ORGANISM: Human
109 <400> SEQUENCE: 10
110 ccacctactg tgaccc                                            16
113 <210> SEQ ID NO: 11
114 <211> LENGTH: 70
115 <212> TYPE: DNA
116 <213> ORGANISM: Human
118 <400> SEQUENCE: 11
119 ttgcctgctc gacttagatc cgcgtctcct ttgatttgta ccactctttt tcggtcaaaa    60
121 acgagatcaa                                                   70
124 <210> SEQ ID NO: 12
125 <211> LENGTH: 71
126 <212> TYPE: DNA
127 <213> ORGANISM: Human
129 <400> SEQUENCE: 12
130 ttgcctgctc gacttagatc cacctactgt gaccctttgt accactcttt ttcggtcaaa    60
132 aacgagatca g                                                 71
135 <210> SEQ ID NO: 13
136 <211> LENGTH: 37
137 <212> TYPE: DNA
138 <213> ORGANISM: Human
140 <400> SEQUENCE: 13
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```
141 taccagctta acacatagca tcactggata gcgacgt                          37
144 <210> SEQ ID NO: 14
145 <211> LENGTH: 73
146 <212> TYPE: DNA
147 <213> ORGANISM: Human
149 <400> SEQUENCE: 14
150 ttgcctgctc gacttagatc cgcgtctcct ttgatttgta ccactctttt tccaataact   60
152 aaaggtacaa cat                                                     73
155 <210> SEQ ID NO: 15
156 <211> LENGTH: 73
157 <212> TYPE: DNA
158 <213> ORGANISM: Human
160 <400> SEQUENCE: 15
161 ttgcctgctc gacttagatc cacctactgt gaccctttgt accactcttt ttcaataact   60
163 aaaggtacaa cac                                                     73
166 <210> SEQ ID NO: 16
167 <211> LENGTH: 37
168 <212> TYPE: DNA
169 <213> ORGANISM: Human
171 <400> SEQUENCE: 16
172 ggcataataa tctccaaaga tcactggata gcgacgt                           37
175 <210> SEQ ID NO: 17
176 <211> LENGTH: 68
177 <212> TYPE: DNA
178 <213> ORGANISM: Human
180 <400> SEQUENCE: 17
181 ttgcctgctc gacttagatc cgcgtctcct ttgatttgta ccactctttt tccagtggtt   60
183 ttccaacg                                                          68
186 <210> SEQ ID NO: 18
187 <211> LENGTH: 70
188 <212> TYPE: DNA
189 <213> ORGANISM: Human
191 <400> SEQUENCE: 18
192 ttgcctgctc gacttagatc cacctactgt gaccctttgt accactcttt ttcacagtgg   60
194 ttttccaaca                                                        70
197 <210> SEQ ID NO: 19
198 <211> LENGTH: 32
199 <212> TYPE: DNA
200 <213> ORGANISM: Human
202 <400> SEQUENCE: 19
203 tgaacacacc gggtatcact ggatagcgac gt                                32
206 <210> SEQ ID NO: 20
207 <211> LENGTH: 18
208 <212> TYPE: DNA
209 <213> ORGANISM: Human
211 <400> SEQUENCE: 20
212 ttgcctgctc gacttaga                                                18
215 <210> SEQ ID NO: 21
216 <211> LENGTH: 18
```

```
217 <212> TYPE: DNA
218 <213> ORGANISM: Human
220 <400> SEQUENCE: 21
221 acgtcgctat ccagtgat                                                   18
224 <210> SEQ ID NO: 22
225 <211> LENGTH: 15
226 <212> TYPE: DNA
227 <213> ORGANISM: Human
229 <400> SEQUENCE: 22
230 ccgcgtctcc tttga                                                      15
233 <210> SEQ ID NO: 23
234 <211> LENGTH: 16
235 <212> TYPE: DNA
236 <213> ORGANISM: Human
238 <400> SEQUENCE: 23
239 ccacctactg tgaccc                                                     16
242 <210> SEQ ID NO: 24
243 <211> LENGTH: 15
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Artificial DNA
250 <400> SEQUENCE: 24
251 catgccaatg acgga                                                      15
254 <210> SEQ ID NO: 25
255 <211> LENGTH: 15
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Artificial DNA
262 <400> SEQUENCE: 25
263 catgcgaatg acggc                                                      15
```

insufficient - what is the source of genetic material? (see item 11 on Error Summary Sheet)

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<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:24,25

VERIFICATION SUMMARY   DATE: 12/03/2005
PATENT APPLICATION: **US/10/665,671**   TIME: 09:47:09

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